

#6

RAW SEQUENCE LISTING

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Application Serial Number: 10/511,627

Source: PCT

Date Processed by STIC: 10/26/04

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DATE: 10/26/2004

PATENT APPLICATION: US/10/511,627

TIME: 17:39:36

Input Set : A:\2923-657.txt

Output Set: N:\CRF4\10262004\J511627.raw

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3 <110> APPLICANT: Eulenberg, Karsten
4     Steuernagel, Arnd
5     Haeder, Thomas
6     Meise, Martin
7     Guenter, Broenner
9 <120> TITLE OF INVENTION: Proteins Involved in the Regulation of Energy Homeostasis
11 <130> FILE REFERENCE: 2923-657
C--> 13 <140> CURRENT APPLICATION NUMBER: US/10/511,627
C--> 13 <141> CURRENT FILING DATE: 2004-10-18
13 <150> PRIOR APPLICATION NUMBER: PCT/EP03/04650
14 <151> PRIOR FILING DATE: 2003-05-02
16 <150> PRIOR APPLICATION NUMBER: EP 02 010 948.4
17 <151> PRIOR FILING DATE: 2002-05-16
19 <150> PRIOR APPLICATION NUMBER: EP 02 010 332.1
20 <151> PRIOR FILING DATE: 2002-05-07
22 <150> PRIOR APPLICATION NUMBER: EP 02 009 883.6
23 <151> PRIOR FILING DATE: 2002-05-02
25 <160> NUMBER OF SEQ ID NOS: 73
27 <170> SOFTWARE: PatentIn version 3.2
29 <210> SEQ ID NO: 1
30 <211> LENGTH: 615
31 <212> TYPE: PRT
32 <213> ORGANISM: Drosophila melanogaster
34 <400> SEQUENCE: 1
36 Leu Val Lys Ile Ala Asn Tyr Gln Asp Leu Leu Gly Ser His His Gln
37 1           5           10           15
40 Leu Leu Ile Ala Ala Thr Ala Ala Ala Ala Ala Ala Ala Glu
41           20           25           30
44 Pro Gln Leu Gln Leu Gln His Leu Leu Pro Ala Ala Pro Thr Thr Pro
45           35           40           45
48 Ala Val Ile Ser Asn Pro Ile Asn Ser Ile Gly Pro Ile Asn Gln Ile
49           50           55           60
52 Ser Ser Ser Ser His Pro Ser Asn Asn Asn Gln Gln Ala Val Phe Glu
53 65           70           75           80
56 Lys Ala Ile Thr Ile Ser Ser Ile Ala Ile Lys Arg Arg Pro Thr Leu
57           85           90           95
60 Pro Gln Thr Pro Ala Ser Ala Pro Gln Val Leu Ser Pro Ser Pro Lys
61           100          105          110
64 Arg Gln Cys Ala Ala Ala Val Ser Val Leu Pro Val Thr Val Pro Val
65           115          120          125
68 Pro Val Pro Val Ser Val Pro Leu Pro Val Ser Val Pro Val Pro Val
69           130          135          140
72 Ser Val Lys Gly Gly His Pro Ile Ser His Thr His Gln Ile Ala His Thr

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73 145          150          155          160
76 His Gln Ile Ser His Ser His Pro Ile Ser His Pro His His His Gln
77          165          170          175
80 Leu Ser Phe Ala His Pro Thr Gln Phe Ala Ala Ala Val Ala Ala His
81          180          185          190
84 His Gln Gln Gln Gln Gln Gln Gln Ala Gln Gln Gln Gln Gln Ala Val
85          195          200          205
88 Gln Gln Gln Gln Gln Gln Ala Val Gln Gln Gln Gln Val Ala Tyr Ala
89          210          215          220
92 Val Ala Ala Ser Pro Gln Leu Gln Gln Gln Gln Gln Gln Gln Gln His
93 225          230          235          240
96 Arg Leu Ala Gln Phe Asn Gln Ala Ala Ala Ala Ala Leu Leu Asn Gln
97          245          250          255
100 His Leu Gln Gln Gln His Gln Ala Gln Gln Gln Gln His Gln Ala Gln
101          260          265          270
104 Gln Gln Ser Leu Ala His Tyr Gly Gly Tyr Gln Leu His Arg Tyr Ala
105          275          280          285
108 Pro Gln Gln Gln Gln Gln His Ile Leu Leu Ser Ser Gly Ser Ser Ser
109          290          295          300
112 Ser Lys His Asn Ser Asn Asn Asn Ser Asn Thr Ser Ala Gly Ala Ala
113 305          310          315          320
116 Ser Ala Ala Val Pro Ile Ala Thr Ser Val Ala Ala Val Pro Thr Thr
117          325          330          335
120 Gly Gly Ser Leu Pro Asp Ser Pro Ala His Glu Ser His Ser His Glu
121          340          345          350
124 Ser Asn Ser Ala Thr Ala Ser Ala Pro Thr Thr Pro Ser Pro Ala Gly
125          355          360          365
128 Ser Val Thr Ser Ala Ala Pro Thr Ala Thr Ala Thr Ala Ala Ala Ala
129          370          375          380
132 Gly Ser Ala Ala Ala Thr Ala Ala Ala Thr Gly Thr Pro Ala Thr Ser
133 385          390          395          400
136 Ala Val Ser Asp Ser Asn Asn Asn Leu Asn Ser Ser Ser Ser Ser Asn
137          405          410          415
140 Ser Asn Ser Asn Ala Ile Met Glu Asn Gln Met Ala Leu Ala Pro Leu
141          420          425          430
144 Gly Leu Ser Gln Ser Met Asp Ser Val Asn Thr Ala Ser Asn Glu Glu
145          435          440          445
148 Glu Val Arg Thr Leu Phe Val Ser Gly Leu Pro Met Asp Ala Lys Pro
149          450          455          460
152 Arg Glu Leu Tyr Leu Leu Phe Arg Ala Tyr Glu Gly Tyr Glu Gly Ser
153 465          470          475          480
156 Leu Leu Lys Val Thr Ser Lys Asn Gly Lys Thr Ala Ser Pro Val Gly
157          485          490          495
160 Phe Val Thr Phe His Thr Arg Ala Gly Ala Glu Ala Ala Lys Gln Asp
161          500          505          510
164 Leu Gln Gly Val Arg Phe Asp Pro Asp Met Pro Gln Thr Ile Arg Leu
165          515          520          525
168 Glu Phe Ala Lys Ser Asn Thr Lys Val Ser Lys Pro Lys Pro Gln Pro
169          530          535          540

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172 Asn Thr Ala Thr Thr Ala Ser His Pro Ala Leu Met His Pro Leu Thr
173 545          550          555          560
176 Gly His Leu Gly Gly Pro Phe Phe Pro Gly Gly Pro Glu Leu Trp His
177          565          570          575
180 His Pro Leu Ala Tyr Ser Ala Ala Ala Ala Glu Leu Pro Gly Ala
181          580          585          590
184 Ala Ala Leu Gln His Ala Thr Leu Val His Pro Ala Leu His Pro Gln
185          595          600          605
188 Val Pro Val Arg Ser Tyr Leu
189          610          615
192 <210> SEQ ID NO: 2
193 <211> LENGTH: 17
194 <212> TYPE: DNA
195 <213> ORGANISM: Mus musculus
197 <400> SEQUENCE: 2
198 cctggatcgc accaacg
201 <210> SEQ ID NO: 3
202 <211> LENGTH: 22
203 <212> TYPE: DNA
204 <213> ORGANISM: Mus musculus
206 <400> SEQUENCE: 3
207 ttaagctgct gttccatgac ca
210 <210> SEQ ID NO: 4
211 <211> LENGTH: 20
212 <212> TYPE: DNA
213 <213> ORGANISM: Mus musculus
216 <220> FEATURE:
217 <221> NAME/KEY: misc_feature
218 <222> LOCATION: (1)..(1)
219 <223> OTHER INFORMATION: FAM reporter dye
221 <220> FEATURE:
222 <221> NAME/KEY: misc_feature
223 <222> LOCATION: (20)..(20)
224 <223> OTHER INFORMATION: TAMRA quencher dye
226 <400> SEQUENCE: 4
227 tccaggctgc catagcgcgc
230 <210> SEQ ID NO: 5
231 <211> LENGTH: 19
232 <212> TYPE: DNA
233 <213> ORGANISM: Mus musculus
235 <400> SEQUENCE: 5
236 cctgccaaacc ctgatcaca
239 <210> SEQ ID NO: 6
240 <211> LENGTH: 20
241 <212> TYPE: DNA
242 <213> ORGANISM: Mus musculus
244 <400> SEQUENCE: 6
245 tttcaatgcc agcgaaagtg
248 <210> SEQ ID NO: 7

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249 <211> LENGTH: 23
250 <212> TYPE: DNA
251 <213> ORGANISM: Mus musculus
254 <220> FEATURE:
255 <221> NAME/KEY: misc_feature
256 <222> LOCATION: (1)..(1)
257 <223> OTHER INFORMATION: FAM reporter dye
259 <220> FEATURE:
260 <221> NAME/KEY: misc_feature
261 <222> LOCATION: (23)..(23)
262 <223> OTHER INFORMATION: TAMRA quencher dye
264 <400> SEQUENCE: 7
265 cgggtggctac agacttgcca cgg                                     23
268 <210> SEQ ID NO: 8
269 <211> LENGTH: 22
270 <212> TYPE: DNA
271 <213> ORGANISM: Mus musculus
273 <400> SEQUENCE: 8
274 agcgggtgggtt ctatgtcgat tt                                     22
277 <210> SEQ ID NO: 9
278 <211> LENGTH: 19
279 <212> TYPE: DNA
280 <213> ORGANISM: Mus musculus
282 <400> SEQUENCE: 9
283 cgggattttag gaaccggct                                           19
286 <210> SEQ ID NO: 10
287 <211> LENGTH: 22
288 <212> TYPE: DNA
289 <213> ORGANISM: Mus musculus
292 <220> FEATURE:
293 <221> NAME/KEY: misc_feature
294 <222> LOCATION: (1)..(1)
295 <223> OTHER INFORMATION: FAM reporter dye
297 <220> FEATURE:
298 <221> NAME/KEY: misc_feature
299 <222> LOCATION: (22)..(22)
300 <223> OTHER INFORMATION: TAMRA quencher dye
302 <400> SEQUENCE: 10
303 aggcgtgaag cccgtgggat ct                                       22
306 <210> SEQ ID NO: 11
307 <211> LENGTH: 21
308 <212> TYPE: DNA
309 <213> ORGANISM: Mus musculus
311 <400> SEQUENCE: 11
312 acaaggatgg caagagcaga g                                         21
315 <210> SEQ ID NO: 12
316 <211> LENGTH: 22
317 <212> TYPE: DNA
318 <213> ORGANISM: Mus musculus

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320 <400> SEQUENCE: 12
321 atggaaattg cttggactgc tt
324 <210> SEQ ID NO: 13
325 <211> LENGTH: 26
326 <212> TYPE: DNA
327 <213> ORGANISM: Mus musculus
330 <220> FEATURE:
331 <221> NAME/KEY: misc_feature
332 <222> LOCATION: (1)..(1)
333 <223> OTHER INFORMATION: FAM reporter dye
335 <220> FEATURE:
336 <221> NAME/KEY: misc_feature
337 <222> LOCATION: (26)..(26)
338 <223> OTHER INFORMATION: TAMRA quencher dye
340 <400> SEQUENCE: 13
341 catgggcact gtcacttttg agcagg
344 <210> SEQ ID NO: 14
345 <211> LENGTH: 914
346 <212> TYPE: PRT
347 <213> ORGANISM: Drosophila melanogaster
349 <400> SEQUENCE: 14
351 Met Glu Val Phe Gln Thr Asp Ser His Tyr Ile Phe Val Lys Arg Asp
352 1 5 10 15
355 Lys Ser Leu Trp Trp His Arg Arg Thr Ser Glu Phe Ser Ile Lys Ala
356 20 25 30
359 Gly Trp Asp Leu Ser Ser Val Asp Asp Ile Glu Cys Ile Gly Val Thr
360 35 40 45
363 His Gly Ile Val Gly Val Ile Ser Leu Pro Asn Val Tyr Glu Pro His
364 50 55 60
367 Leu Val Val Val Lys Glu Ala Ser Ala Val Gly Val Leu Tyr Pro Pro
368 65 70 75 80
371 His Leu Val Tyr Lys Ile Lys Ser Ile Cys Ile Leu Ser Ala Asp Asp
372 85 90 95
375 Pro Asp Thr Asp Leu Pro Asn Cys Thr Lys His Thr Lys Ser Asn Gln
376 100 105 110
379 Ser Thr Pro Thr His Ser Val Ser Thr Ser Asn Asn Asn Ala Ser
380 115 120 125
383 Val Pro Ser Ser Gly Gly Gly Ser Ser Lys Ser Thr Lys Leu Phe Glu
384 130 135 140
387 Gly Met Asn Lys Thr Trp Gly Ala Val Lys Ser Ala Gly Asn Thr Ile
388 145 150 155 160
391 Lys Asn Thr Thr Gln Gln Ala Ala Asn Leu Ala Thr Lys Gln Val Lys
392 165 170 175
395 Ser Ser Val Gly Ile Arg Glu Pro Arg His Ile Glu Arg Arg Ile Thr
396 180 185 190
399 Glu Glu Leu His Lys Ile Phe Asp Glu Thr Asp Ser Phe Tyr Phe Ser
400 195 200 205
403 Phe Asp Cys Asp Ile Thr Asn Asn Leu Gln Arg His Glu Ala Lys Ser
404 210 215 220

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L:13 M:270 C: Current Application Number differs, Replaced Current Application No

L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date